

1 **Supplementary Text**

2 **Genome assembly of strain α 710.** The genome of α 710 consisting of five contigs
3 381317 bp, 278435 bp, 867911 bp, 98253 bp, 616977 bp in size, respectively, was assembled
4 using the genome of MC58 as a reference. The order of the contigs was verified by gap-
5 spanning PCRs. With respect to the reference genome of strain MC58, the first sequencing
6 gap of about 3.0 kb is located between NMB0323 and NMB0326 and comprises the two
7 genes NMB0324 (*rpmA*) and NMB0325 (*rplU*) on the MC58 chromosome. Similarly, the
8 second gap of about 8.0 kb lies between NMB0583 and NMB0585 and covers NMB0584
9 (FrpC operon protein), and the third gap spans approximately 5.0 kb between NMB0960 and
10 NMB0962 corresponding to NMB0961 (*funZ*) and is located in a non-homologous region.
11 The fourth gap corresponding to approx. 1.6 kb between NMB1541 (*lbpB*) and NMB1553
12 (transposase) contains the genes NMB1542 to NMB1552 being identical to the neisserial
13 filamentous prophage Nf1-B1 (7). Finally, the fifth gap spans a region of about 1.4 kb on the
14 MC58 chromosome and is located between NMB2103 (*pyrH*) and NMB2104 (*mafA-3*).

15 **Comparison of the serogroup B *maf* loci.** With respect to the numbering used for strain
16 MC58 (14) both serogroup B genomes contain three loci termed *maf-1* to *maf-3* (Fig. 2 and
17 S3). Each individual *maf* locus comprises a co-oriented tandem of a *mafA* and a *mafB* gene,
18 where *mafA* was shown to code for an outer membrane protein (16) and *mafB* was predicted
19 to encode a secreted or membrane bound protein in *N. meningitidis* (8) and to be involved in
20 adhesion to epithelial cells in *N. gonorrhoeae* (9), respectively. Although the *mafA* genes
21 seem to be quite conserved and show little sequence variability, at each *maf* locus there is a
22 number of silent gene cassettes encoding alternative MafB C-termini thus enabling a marked
23 C-terminal sequence variability for MafB (1). A comparison of the *maf* loci in the two
24 genomes shows that while *maf-2* is almost identical in both strains there are considerable
25 differences in the genetic structure of *maf-1* and *maf-3* with respect to the number of silent

1 gene cassettes. In addition, in both strains there is an additional *mafB* gene upstream of the
2 *maf-2* locus designated *mafB-2'* in Fig. S3A not present in the other *maf* loci. As can be
3 further seen in Fig. S3, in the two sequenced serogroup B genomes (as well as in the other
4 meningococcal genomes sequenced so far, unpublished) the number of silent *mafB* cassettes
5 decreases with increasing distance to *oriC*. In rapidly dividing bacteria like *N. meningitidis*
6 replication re-initiation might occur prior to the separation of the daughter strands thus
7 generating a gene copy number gradient from *oriC* to *terC* (10). Since *maf-3* is the *maf* locus
8 closest to *oriC*, this would result in a higher probability for recombination between the silent
9 3'-cassettes on the replicated sister strands when compared to the more distant *maf* loci and
10 would thus facilitate the expansion seen for the silent 3' cassettes at the *maf-3* locus. In
11 addition, there would also be a higher copy number for *mafB-3* than for the other *mafB* genes
12 per cell, and since only *mafB-3* starts with a canonical ATG codon whereas *mafB-2'* starts
13 with the non-canonical TTG and *mafB-1* as well as *mafB-2* both with a GTG codon this would
14 result in higher expression levels for the encoded MafB-3 protein. The orthologous MafB-3
15 proteins are quite similar to each other but differ considerably from the other paralogous
16 MafB proteins in both strains (Fig. S3) which in turn are very similar to each other despite
17 their variant C-termini.

18 Similar to the *pilE* locus, the genetic make-up of the *maf* loci therefore suggests that the
19 encoded MafB-proteins might be involved in host interactions. In particular, the close location
20 of *maf3* to *oriC* comparable to that of the *pilE* locus (Fig. 2) and the sequence difference
21 between the encoded MafB proteins (Fig. S3B) further indicate that MafB-3 on the one hand
22 and MafB-1 and MafB-2 on the other hand, might have different functions. However, in
23 contrast to PilE or the TPS and RTX proteins (2, 15, 17), there are currently no experimental
24 data on the potential role of MafB for the interaction of *N. meningitidis* with human host cells.

1 **Comparison of the MC58 and α 710 virulence gene content.** Of the 104 putative
2 pathogenicity genes identified through homology matches with unknown virulence genes in
3 strain MC58 by Tettelin *et al.* (14), 97 also present in strain α 710. Six genes, *lgtG*
4 (NMB2032) encoding a lipopolysaccharide glycosyl transferase, *opc* encoding the class 5
5 outer membrane protein Opc, NMB0393 encoding a small multidrug resistance protein
6 (IPR000390), *nadA* (NMB1994) encoding the minor adhesin NadA, as well as NMB1210
7 coding for putative RTX activating enzyme and NMB1214 encoding TpsA3 are entirely
8 missing in α 710. The three genes NMB0293, NMB1346 and NMB1449 all encode putative
9 TonB-dependent siderophor receptors. NMB0293 is a pseudogene in α 710 (NMBB_0325A)
10 whereas NMB1346 is a pseudogene in MC58 and α 710 contains a functional ortholog
11 (NMBB_1488). NMB1449 is a pseudogene in MC58 and the ortholog in α 710 (NMBB_1611)
12 is inactivated due to an insertion of IS*Nme1* transposase. Of the four phase-variably expressed
13 opacity protein *opa* encoding genes, three are in an off state in both strains, and both contain 8
14 silent *pilS* cassettes with albeit differing sequences. However, the orthologs of candidate
15 pathogenicity genes as identified by Tettelin *et al.* have overall no higher sequence variability
16 with each other (BSR = 0.990, CI_{0.95} = [0.671, 1.00]) than non-pathogenicity genes (BSR =
17 0.990, CI_{0.95} = [0.774, 1.000]) (*p* = 0.3554, Wilcoxon test).

18 From a set of 60 potential core pathogen-specific genes that were found to be absent in *N.*
19 *lactamica* but present in all isolates in a panel of 48 meningococcal strains via mCGH by
20 Dunning Hotopp *et al.* (6), all were present also in strain α 710 although one gene, NMB0715
21 encoding the central part of a potassium/proton antiporter, has been inactivated due to the
22 integration of an IS1655 element in α 710. Likewise, of the 45 genes recently found in another
23 mCGH study by Stabler *et al.* (12) to be absent in 7 commensal *Neisseria* species but present
24 in all 18 serogroup B meningococcal strains investigated and that do not code for IS elements,
25 only 3 are missing in α 710: again NMB0293, NMB0832 which codes for a putative anticodon
26 nuclease, and NMB1167 encoding a small hypothetical protein.

1 **Supplemental figure legends:**

2 **Fig. S1:** Growth curves of strains MC58 (green) and α 710 (blue) in (A) NDM and (B) RPMI
3 medium.

4 The dots are the measured OD₆₀₀ values and the solid lines with the same colors are the
5 corresponding estimated logistic growth curves which were consecutively used for
6 determining the growth rates for both strains from three independent experiments.

7 **Fig. S2:** Multiple whole-genome alignment of six sequenced meningococcal genomes using
8 Mauve 2.3.0 (4).

9 For each genome, the order of locally collinear blocks (LCBs) is given as a series of coloured
10 blocks with the putative origin of replication designated *oriC* being indicated by a black
11 rectangle. LCBs identically present in the six genomes are given in the same colours and
12 horizontally flipped LCBs identify chromosomal inversions with respect to the genome of
13 α 14. Gaps or white spaces in the LCB order image indicate regions not (identically) present in
14 all four genomes. For sake of clarity, only the annotations for the two serogroup B genomes
15 MC58 and α 710 are given. They are largely collinear and share a large chromosomal
16 inversion spanning almost half of the entire genome (marked by a horizontal black double-
17 headed arrow in the respective panels) which is flanked on both sides by IHT-B and IHT-C,
18 respectively, when compared to the other four genomes. Similar to figure 2, also the three
19 inversions coupled to translocations IT1 – IT3 are indicated as well as the α 710-specific P2-
20 like prophage (P2).

21 **Fig. S3.** Comparison of the *maf* loci in the two meningococcal serogroup B genomes.

22 **(A)** Genetic organization of the *maf* loci in the genomes of the two sequenced serogroup B
23 strains MC58 and α 710. Each locus contains a *mafA* (white arrow) and a *mafB* (black arrow)
24 gene together with a number of adjacent *mafB* 3'-terminal gene cassettes (dark grey arrow).
25 Of note, the *maf3* locus contains a *mafA* pseudogene (dashed white arrow) and has the highest
26 number of silent *mafB* cassettes. Upstream of *mafA*-2 is another *mafB* gene termed *mafB*-2'

1 which is thus not part of the *maf2* locus. CDS not coding for *mafB* gene cassettes are indicated
2 by light grey arrows. Identical regions in both genomes are connected by grey vertical/oblique
3 areas/lines. The loci are given from top to bottom with increasing distance to *oriC* (see also
4 Fig. 2). For the MC58 loci, the corresponding gene identifiers are given below the arrows.

5 **(B)** Neighbor joining tree based on the multiple sequence alignment of the encoded MafB
6 proteins in the two serogroup B genomes. For phylogenetic analyses of the MafB proteins the
7 corresponding amino acid sequences were first aligned using MUSCLE (5) and alignment
8 gaps were removed from the obtained multiple sequence alignment (MSA) using Gblocks (3)
9 with default parameters. From the de-gapped MSA comprising 259 amino acids in 6 blocks, a
10 bootstrap consensus tree with 100 replicates was constructed using MEGA4 (13) based on the
11 neighbor joining method. The long branch leading to MafB-3 indicates an elevated level of
12 sequence divergence from the other MafB proteins. Numbers indicate the percent bootstrap
13 support.

14

1 **Table S1.** Genes and primers used for real-time RT-PCR.

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Primer	Sequence (5'-3')
aroB RT(F)	CAACCTCATTTGACGGGCTGA
aroB RT(R)	GTCGGTATTGAACGAACGGTGC
NMB0085_F (RT)	CGTACGGCGTGAGCTCAAATTT
NMB0085_R (RT)	CAAGATAAAATCCGCCACAATCG
NMB0208_RT(R)	GGATGCAGTCGACGGGCAGGGG
NMB0341 RT (F)	CAAAGGCGAAACGGTCAAACAGA
NMB0341 RT (R)	AGATTCGGAATGTGAAGCACGCT
NMB1048_RT(F)	CCGCCGCGTTATCTTATTGGTA
NMB1048_RT(R):	GCAGACCTAAAACCGCAATCGAA
NMB1104_RT(F)	GCCAAAGCCTTGAGCAACCATA
NMB1104_RT(R)	TTGTACCAAGCACAGGTCATGCG
NMB1540_F (RT)	AAACATCAGCACGGTGAAATCG
NMB1540_R (RT)	GGTTTTTACTGCCGTAGGCGGTT
NMB1592_RT (F)	CCCCGTGAATCCTATCAATACCG
NMB1592_RT(R)	CCGCCTGAACCTTGGTCATTAA
NMB1845_F (RT)	GGCTTCCGACTGTCAACGATGA
NMB1845_R (RT)	CTGAAAAATTCTGTGCGCGAAGC
NMB2113_RT(F)	GBAATTAGAGAAGCCGCATTACC
NMB398_F (RT)	CAATACCGCTCCACACCATACTC
NMB398_R (RT)	ATTCGATAATGCGGTGGTAACGC
NMB994_F (RT)	ACCTTTCACTGCCTGGTCA
NMB994_R (RT)	GGCAAGGTGTTGACGGTATTGG
NMB995_F (RT)	GCGTTTACCAAGAAGTCGGCAA
NMB995_R (RT)	CAGGAGTTTTTCAGGGTTGCGA

4

1 **Table S2.** The 1% most variable proteins from the core genome of strains α 710 and MC58.
2

MC58	BSR	PSORTb ⁽¹⁾	COG ⁽²⁾	InterPro entries ⁽³⁾	Putative gene product/function
NMB0397	0.19	UK	X	-	Hypothetical protein
NMB0497	0.47	OM	U	IPR008619/IPR008638 and IPR006914/IPR006915	Hemagglutinin-related TPS system protein HrpA1
NMB0499	0.60	UK	U	IPR006914/IPR006915	HrpA alternative C-terminal cassette
NMB0655	0.57	UK	X	IPR008106	MafB-3 alternative C-terminal cassette
NMB0664	0.49	UK	X	-	Hypothetical protein
NMB0846	0.58	CP	M	IPR001296	Glycosyl transferase
NMB0865	0.39	CM	X	-	Hypothetical membrane protein
NMB0971	0.56	UK	X	-	Hypothetical protein
NMB1087	0.57	UK	X	-	Hypothetical lipoprotein
NMB1157	0.55	UK	X	-	Hypothetical protein
NMB1281	0.55	UK	K	IPR004576	Transcription-repair coupling factor
NMB1541	0.53	OM	R	IPR001677	Transferrin binding protein
NMB1772	0.47	UK	U	IPR006914 and IPR006915	HrpA alternative C-terminal cassette
NMB1826	0.60	CP	S	IPR002942	RNA-binding S4
NMB1837	0.38	UK	X	-	Hypothetical protein
NMB1883	0.55	UK	X	-	Hypothetical protein
NMB1931	0.60	CP	S	IPR007416	Protein of unknown function DUF469

3 ⁽¹⁾ For the abbreviations of the PSORTb predictions for the protein sub-cellular localization the reader is referred to the legend of figure 3.4 ⁽²⁾ For the abbreviations of the COG functional categories the reader is referred to the legend of figure 3.5 ⁽³⁾ The InterPro database entries are given for each protein for further information on the respective protein families.

1 **Table S3.** Novel putative cMMEs and MMEs as identified by pairwise comparisons of the
 2 two serogroup B meningococcal genomes. Assignments are based on the criteria given in
 3 (11).

4

Site	Gene content in MC58	Gene content in a710
cMME <i>bfrAlipA</i>	putative FrpA/C-activating lysine-acyltransferase, haemagglutinin/hemolysin-related protein TpsA3' and hypothetical proteins (NMB1209-1215)	-
cMME <i>gluQtal</i>	conserved hypothetical protein (NMB0350)	-
cMME <i>hemYhemE</i>	conserved hypothetical protein (NMB0780)	-
cMME <i>mtgrgmhB</i>	<i>lgtG</i> pseudogene	-
cMME <i>nadAnicB</i>	putative small multidrug resistance protein (NMB0393)	-
cMME <i>pyrC</i>	-	putative lipoprotein (NMBB_0762)
cMME <i>pyrD</i>	-	hypothetical proteins (NMBB_0244-5)
cMME <i>scpa</i>	hypothetical integral membrane protein (NMB1502)	-
cMME <i>thiEthiS</i>	-	Zn-dependent oxidoreductase (NMBB_2379) (IPR014182) and HxlR type HTH transcriptional regulator (NMBB_2381) (IPR002577)
MME <i>alaS</i>	hypothetical proteins (NMB1596-1600) and a IS <i>Nme1</i> (NMB1601) and a truncated IS <i>110</i> family transposase (NMB1602)	type II RM system Ngo14ORF1425P (NMBB_1827/1828)
MME <i>hrpA</i>	putative HTH transcriptional regulator (IPR001387) and two conserved hypothetical proteins (NMB2012-2014)	AAA+ type ATPase (IPR003593) and protein with a von Willebrand factor, type A, domain (IPR002035) (NMBB_2310/2311)
MME <i>pglC</i>	<i>pglB</i>	glycosyltransferases (NMBB_2071-2074)
MME <i>prpCacnA</i>	conserved hypothetical integral membrane protein (NMB0432)	<i>vanX</i> -NMBB_0475
MME <i>topA</i>	hypothetical proteins (NMB0119/0020)	hypothetical proteins (NMBB_0125/0126)

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6

1 **Table S4.** Functional categories over or under represented in the core genes regulated upon
2 adhesion to epithelial cell. (The odds ratio (OR) as well as the 2.5 and 97.5 percentiles are
3 given based on Fisher's exact test together with the FDR after multiple testing correction
4 according to BH.)

5

	OR	2.5%	97.5%	FDR
Core genes regulated in both strains				
Metabolism	2.34	1.07	5.26	0.077
Not in COGs	0.10	0.01	0.47	0.003
Core genes regulated only in MC58				
Metabolism	2.71	1.72	4.31	2.50E-05
Not in COGs	0.10	0.03	0.25	0.000
Core genes regulated only in <i>a710</i>				
Inforamtion storage and processing	2.18	1.04	4.69	0.096
Metabolism	2.07	0.98	4.47	0.071
Poorly characterized	0.36	0.12	0.98	0.076
Not in COGs	0.10	0.01	0.47	0.004

6

7

1 **Table S5.** Core genes regulated upon adhesion to human FaDu nasopharyngeal cell lines. Only genes having a FDR less than 0.05 and a greater
 2 than 80% probability of being differentially regulated based on the B-statistic under the various conditions tested were considered.

MC58	Gene	Product	MC_Adh_RPMI	a710_Adh_RPMI	MC_Adh-aAdh
NMB0005		putative arsenate reductase	-1,50	-1,18	
NMB0009		putative BolA-like protein	1,34		
NMB0011	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1,83	1,31	
NMB0017	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase		1,05	
NMB0018	<i>pilE</i>	major pilin PilE		0,75	-0,68
NMB0020	<i>pilS2</i>	pilS2 cassette			-1,17
NMB0023	<i>pilS5</i>	pilS5 cassette	1,73		
NMB0025	<i>pilS7</i>	pilS7 cassette	1,58		
NMB0027	<i>fkbP</i>	FK506-binding protein (peptidyl-prolyl cis-trans isomerase; PPIase; rotamase)	-1,08		
NMB0029		putative D-3-phosphoglycerate dehydrogenase (PGDH)	-1,25		
NMB0031	<i>glmS</i>	glucosamine--fructose-6-phosphate aminotransferase			-0,66
NMB0032		hypothetical lipoprotein	-2,35		
NMB0034		conserved hypothetical integral membrane protein	-2,11	-1,75	-1,29
NMB0035		conserved hypothetical lipoprotein	-2,50	-1,16	-1,45
NMB0036		putative Tat-translocated enzyme	-2,13	-1,37	-1,23
NMB0050		conserved hypothetical integral membrane protein		1,03	
NMB0053		conserved hypothetical protein	-1,35		
NMB0054		hypothetical lipoprotein	-1,31		
NMB0055	<i>proC</i>	pyrroline-5-carboxylate reductase (P5CR; P5C reductase)	-1,25		
NMB0057		ComE-like protein	-1,29		
NMB0060		putative oligopeptide transporter	-1,87	-1,78	
NMB0064	<i>galE</i>	UDP-glucose 4-epimerase (galactowaldenase; UDP-galactose 4-epimerase)	2,06	1,59	
NMB0065		conserved hypothetical protein	-2,63	-1,41	-1,25
NMB0068	<i>siaC</i>	sialic acid synthase		-0,81	0,99
NMB0069	<i>siaB</i>	N-acylneuraminate cytidylyltransferase			1,01
NMB0071	<i>ctrA</i>	polysialic acid capsule export outer-membrane lipoprotein CtrA	1,51		
NMB0072	<i>ctrB</i>	polysialic acid capsule export inner-membrane protein CtrB	1,90		
NMB0074	<i>ctrD</i>	polysialic acid capsule export ATP-binding protein CtrD	1,44		
NMB0075		putative RNA-binding protein	1,43		
NMB0077	<i>damH'</i>	truncated adenine-specific methyltransferase (N-terminal third of the protein)		-1,35	

NMB0085	<i>gltS</i>	sodium/glutamate symport carrier protein (glutamate permease)	-2,56	-1,70	
NMB0086		hypothetical lipoprotein			-0,73
NMB0089	<i>pykA</i>	pyruvate kinase II (PK-2)	1,01		
NMB0091		putative bacteriocin/pheromone	-1,51		
NMB0095		hypothetical protein	-1,89		
NMB0104		hypothetical protein	-1,43		
NMB0106	<i>pyrB</i>	aspartate carbamoyltransferase (aspartate transcarbamylase; ATCase)	1,53		
NMB0107	<i>pyrI</i>	aspartate carbamoyltransferase regulatory chain	1,84	1,01	
NMB0112	<i>rmsB</i>	ribosomal RNA small subunit methyltransferase B		0,93	
NMB0114		putative two-component system sensor protein		0,81	
NMB0115		putative two-component system transcriptional regulator protein	0,98		
NMB0116	<i>smf</i>	Smf protein (DNA processing chain A)	1,58		
NMB0117		conserved hypothetical protein	-0,83		
NMB0118	<i>topA</i>	DNA topoisomerase I (Omega-protein; relaxing enzyme; untwisting enzyme; swivelase)	-1,02		
NMB0119		hypothetical protein	-2,81		
NMB0120		hypothetical integral membrane protein	-3,87		
NMB0124	<i>tuf</i>	elongation factor Tu (EF-Tu)		0,69	-0,68
NMB0127	<i>rplK</i>	50S ribosomal protein L11		0,95	-0,56
NMB0131	<i>rplL</i>	50S ribosomal protein L7/L12		0,39	-0,41
NMB0132	<i>rpoB</i>	DNA-directed RNA polymerase beta chain	1,28		
NMB0133	<i>rpoC</i>	DNA-directed RNA polymerase beta' chain	1,01	1,04	
NMB0136	<i>rpsL</i>	30S ribosomal protein S12		0,58	-0,57
NMB0139	<i>tuf</i>	elongation factor Tu (EF-Tu)		0,75	-0,68
NMB0140	<i>rpsJ</i>	30S ribosomal protein S10	0,84	1,03	
NMB0143	<i>rplD</i>	50S ribosomal protein L4		0,92	-0,54
NMB0144	<i>rplW</i>	50S ribosomal protein L23		0,84	
NMB0145	<i>rplB</i>	50S ribosomal protein L2		0,84	-0,68
NMB0146	<i>rpsS</i>	30S ribosomal protein S19		0,82	-0,68
NMB0147	<i>rplV</i>	50S ribosomal protein L22		0,77	-0,68
NMB0149	<i>rplP</i>	50S ribosomal protein L16		0,69	-0,62
NMB0151	<i>rpsQ</i>	30S ribosomal protein S17		0,63	-0,56
NMB0153	<i>rplX</i>	50S ribosomal protein L24		0,64	
NMB0155	<i>rpsN</i>	30S ribosomal protein S14		0,47	
NMB0157	<i>rplF</i>	50S ribosomal protein L6		0,79	-0,68
NMB0158	<i>rplR</i>	50S ribosomal protein L18		0,75	-0,68
NMB0159	<i>rpsE</i>	30S ribosomal protein S5		0,52	
NMB0162	<i>secY</i>	preprotein translocase SecY subunit		0,62	
NMB0165	<i>rpsM</i>	30S ribosomal protein S13		0,95	
NMB0167	<i>rpsD</i>	30S ribosomal protein S4		0,76	-0,70
NMB0175	<i>zupT</i>	zinc transporter ZupT	-2,52		

NMB0181	<i>skp</i>	periplasmic chaperone Skp (OmpH)	-0,94		
NMB0182	<i>omp</i>	outer-membrane protein assembly factor Omp85	-0,84	0,67	
NMB0192	<i>rnhB</i>	ribonuclease HII (RNase HII)	2,14		
NMB0193	<i>gidA</i>	glucose-inhibited division protein A	1,71		
NMB0196	<i>rne</i>	ribonuclease E (RNase E)	1,78		
NMB0198	<i>rluC</i>	ribosomal large subunit pseudouridine synthase C	-1,31		
NMB0200		conserved hypothetical protein		1,07	
NMB0203	<i>dapB</i>	dihydrodipicolinate reductase (DHPR)	1,47		
NMB0208		putative ferredoxin	2,14	3,16	-1,64
NMB0209		putative glutathione-regulated potassium-efflux system protein (K(+)/H(+) antiporter)	1,04		
NMB0213		putative Sm-like integral membrane protein	0,74	0,86	
NMB0217	<i>rpoN'</i>	truncated RNA polymerase sigma-54 factor	-1,01		
NMB0219	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase II		-0,86	
NMB0230		putative allophanate hydrolase subunit 1 (AHS1)	-1,83		
NMB0237		conserved hypothetical protein	-1,59		
NMB0255		putative cell filamentation protein Fic	-0,99		
NMB0263		putative GTPase EngC			1,10
NMB0266		conserved hypothetical periplasmic protein	1,61		
NMB0267		putative RlpA-like protein	2,59	2,10	
NMB0277		putative MviN-like protein	1,21		1,08
NMB0282		putative exoribonuclease II (ribonuclease II; RNase II)			-1,03
NMB0293		putative TonB-dependent receptor	-3,91		
NMB0296		putative cytochrome C biogenesis protein	-2,26	-1,69	
NMB0299	<i>comE1</i>	DNA-binding competence protein ComE1	3,43		
NMB0310		conserved hypothetical integral membrane protein	1,38		
NMB0316		conserved hypothetical integral membrane protein	1,47		
NMB0317		putative GTP cyclohydrolase I (GTP-CH-I)	1,09		
NMB0322	<i>rpmG</i>	50S ribosomal protein L33		1,10	-1,66
NMB0326	<i>ispB</i>	octaprenyl-diphosphate synthase	1,22		
NMB0330		putative UPF0243 zinc-binding protein	2,18		
NMB0332	<i>pilD</i>	type IV prepilin-like proteins leader peptide processing enzyme PilD	1,69		
NMB0335	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase			0,98
NMB0338		conserved hypothetical integral membrane protein	1,11		
NMB0341	<i>tspA</i>	TspA protein	-1,21		-1,20
NMB0346		conserved hypothetical protein	0,69	0,74	
NMB0351	<i>tal</i>	transaldolase			1,18
NMB0354		conserved hypothetical membrane protein			0,84
NMB0364	<i>frpD</i>	FrpA/C-binding lipoprotein	-1,30		
NMB0365		truncated FrpA/C protein (N-terminal 4% of the protein)	-2,46		
NMB0367		hypothetical protein	-2,31		

NMB0368		hypothetical protein	-2,30		
NMB0369		conserved hypothetical protein	-2,54		
NMB0370		hypothetical protein	-2,72		
NMB0371		hypothetical protein	-3,38		
NMB0372		conserved hypothetical protein	-2,69		
NMB0373		hypothetical protein	-2,73		
NMB0374	<i>mafB1</i>	MafB1 protein	-4,04		
NMB0375	<i>mafA1</i>	MafA1 lipoprotein	-1,45		
NMB0378		putative phosphate permease	-1,51	-1,13	
NMB0379	<i>hemN</i>	oxygen-independent coproporphyrinogen III oxidase		1,15	
NMB0380		putative HTH-type transcriptional regulator	1,11	0,79	
NMB0382	<i>rmpM</i>	outer-membrane protein class 4			-0,64
NMB0386	<i>pgpA</i>	phosphatidylglycerophosphatase A	1,11		1,17
NMB0387		putative ABC transporter ATP-binding protein	-1,58	-0,86	
NMB0389	<i>galM</i>	aldose 1-epimerase (mutarotase)	-2,35		
NMB0393		putative small multidrug resistance protein	-2,84		
NMB0395		conserved hypothetical protein		-1,39	
NMB0398		putative HTH-type transcriptional regulator	2,67	2,55	1,18
NMB0399	<i>xthA</i>	exodeoxyribonuclease III (exonuclease III; EXO III)	2,65	1,73	1,12
NMB0400		truncated IS110 family transposase (C-terminal half of the protein)	1,85	1,34	
NMB0405		putative Mg chelatase-like protein	-1,80		
NMB0406		putative cell division protein FtsN		-1,05	
NMB0408	<i>uppP</i>	undecaprenyl-diphosphatase	-1,90		
NMB0410		putative MraZ-like protein		-0,74	
NMB0412		putative FtsL-like periplasmic protein			0,65
NMB0414	<i>murE</i>	UDP-N-acetyl muramoyl-L-glutamate--2,6-diaminopimelate ligase	1,47		
NMB0416	<i>murF</i>	UDP-N-acetyl muramoyl-tripeptide--D-alanyl-D-alanine ligase	-1,03	-0,64	
NMB0419		conserved hypothetical TPR-containing periplasmic protein		-0,81	
NMB0431	<i>pprC</i>	2-methylcitrate synthase (methylcitrate synthase; citrate synthase 2)		1,51	
NMB0446	<i>pheA</i>	P-protein [includes: chorismate mutase (CM) and prephenate dehydratase (PDT)]	1,28		
NMB0448	<i>pdxJ</i>	pyridoxal phosphate biosynthetic protein PdxJ (PNP synthase)	1,62		
NMB0453		putative mutator MutT protein		1,06	
NMB0454		hypothetical protein	1,12		
NMB0456	<i>amiC</i>	N-acetylmuramoyl-L-alanine amidase AmiC	1,18	1,08	
NMB0459		conserved hypothetical protein	-0,89		
NMB0460	<i>tbp</i>	transferrin-binding protein 2 (TbpB)		-1,83	
NMB0461	<i>tbp</i>	transferrin-binding protein 1 (TbpA)	-1,67	-1,50	
NMB0462		putative spermidine/putrescine-binding lipoprotein	-2,06	-1,22	
NMB0464		putative phospholipase A1	2,48	1,55	
NMB0465		conserved hypothetical integral membrane protein	1,91	1,29	

NMB0466	<i>aspS</i>	aspartyl-tRNA synthetase (aspartate--tRNA ligase; AspRS)	1,90	1,16
NMB0467		hypothetical periplasmic protein	-1,89	
NMB0470		putative transporter	-1,14	
NMB0480		truncated TspB-like protein (N-terminal third of the protein)	-2,24	-1,09
NMB0481		hypothetical protein	-2,85	-1,78
NMB0483		hypothetical integral membrane protein	-2,68	
NMB0488		conserved hypothetical protein	-1,63	
NMB0491		hypothetical protein	-1,76	
NMB0492		conserved hypothetical protein	-2,52	
NMB0497	<i>tpsA2</i>	haemagglutinin/hemolysin-related protein TpsA2	-1,73	
NMB0498		hypothetical protein	-2,20	
NMB0500		hypothetical protein	-3,01	
NMB0503		hypothetical protein	-2,44	
NMB0507		conserved hypothetical protein	-1,51	
NMB0509	<i>tpsS5</i>	putative TpsS5 cassette	-1,06	
NMB0510		conserved hypothetical protein	-2,74	
NMB0512		hypothetical integral membrane protein	-0,90	
NMB0521		hypothetical periplasmic protein	-1,17	-1,12
NMB0526		conserved hypothetical protein	1,55	
NMB0528		conserved hypothetical integral membrane protein	1,53	
NMB0529		conserved hypothetical protein		1,69
NMB0531		putative Na+/H+ antiporter		0,92
NMB0532		putative Do-like serine protease	-1,23	
NMB0533	<i>nth</i>	endonuclease III (DNA-(apurinic or apyrimidinic site) lyase)		0,97
NMB0536		putative Na(+)/H(+) antiporter	-1,36	-1,55
NMB0538		conserved hypothetical protein	0,87	0,83
NMB0539	<i>hemC</i>	porphobilinogen deaminase	1,26	0,97
NMB0540	<i>aspC</i>	aspartate aminotransferase		-1,00
NMB0542		conserved hypothetical protein	-1,86	
NMB0543		putative L-lactate permease	-2,42	-1,44
NMB0546		putative alcohol dehydrogenase (ADH-HT)		1,54
NMB0547	<i>pilV</i>	minor pilin PilV		0,91
NMB0548		putative membrane fusion protein		1,05
NMB0549		putative ABC transporter ATP-binding protein	2,15	
NMB0552		conserved hypothetical integral membrane protein	2,19	
NMB0555		hypothetical membrane-associated protein		1,76
NMB0557		conserved hypothetical protein	-1,45	-1,26
NMB0559		putative ubiquinone biosynthesis protein UbiB		-1,55
NMB0561	<i>grpE</i>	protein GrpE (HSP-70 cofactor)	-0,75	-0,83
NMB0562		conserved hypothetical membrane-associated protein	-1,28	-0,91
				-1,07

NMB0566	<i>nqrD</i>	Na(+) -translocating NADH-quinone reductase subunit D			1,27
NMB0567	<i>nqrC</i>	Na(+) -translocating NADH-quinone reductase subunit C	1,38		2,05
NMB0568	<i>nqrB</i>	Na(+) -translocating NADH-quinone reductase subunit B			1,13
NMB0578		truncated NosD-like protein (C-terminal 90% of the protein)	-1,45		
NMB0581		putative electron transfer flavoprotein-ubiquinone oxidoreductase	0,97		
NMB0583		IS1016 group transposase	-1,15		
NMB0586		putative ABC transporter substrate-binding protein	-1,64	-1,45	-0,91
NMB0588		putative ABC transporter ATP-binding protein		0,93	-1,62
NMB0593		conserved hypothetical protein	1,47		
NMB0594		putative two-component system sensor protein	1,03		
NMB0595		putative two-component system transcriptional regulator protein	0,96		
NMB0597		conserved hypothetical integral membrane protein		-1,16	
NMB0601	<i>tatA/E</i>	sec-independent protein translocase TatA/E component	-1,51	-1,42	
NMB0602		putative HitA-like protein		-0,83	
NMB0603	<i>hisE</i>	phosphoribosyl-ATP pyrophosphatase (PRA-PH)	-0,94		
NMB0604		putative zinc-type alcohol dehydrogenase	-1,60	-1,58	
NMB0605		putative deacetylase	-1,32		-1,98
NMB0606		conserved hypothetical periplasmic protein		-0,86	0,63
NMB0608	<i>secF</i>	preprotein translocase SecF subunit	-1,30	-0,88	
NMB0609	<i>rpsO</i>	30S ribosomal protein S15		0,75	-0,68
NMB0610		putative spermidine/putrescine transport system ATP-binding protein	1,33		
NMB0611		putative spermidine/putrescine transport system permease protein	1,47		
NMB0615		putative ammonium transporter	1,85		0,81
NMB0623		putative spermidine/putrescine-binding lipoprotein	-1,15		
NMB0633	<i>fbpB</i>	iron(III)-transport system permease protein FbpB	0,98	0,86	
NMB0634	<i>fbpA</i>	iron(III)-transport system iron-binding protein FbpB		0,56	-0,49
NMB0637	<i>argH</i>	argininosuccinate lyase (arginosuccinase; ASAL)			1,03
NMB0638	<i>galU</i>	UTP--glucose-1-phosphate uridylyltransferase	1,09		1,30
NMB0640		hypothetical membrane-associated protein	1,06		1,34
NMB0642	<i>ntpA</i>	dATP pyrophosphohydrolase	1,54		
NMB0646		barstar (ribonuclease inhibitor)			-1,53
NMB0647		conserved hypothetical protein			-1,22
NMB0653	<i>mafB2</i>	MafB2 protein	-3,76	-2,23	
NMB0654		conserved hypothetical protein	-2,59	-1,23	-1,40
NMB0656		hypothetical protein	-1,98		
NMB0660		conserved hypothetical protein	-2,85	-1,59	
NMB0667		conserved hypothetical periplasmic protein	-1,80		-1,33
NMB0671		putative NADP-dependent malic enzyme (NADP-ME)		-0,88	
NMB0676		hypothetical protein	0,96		
NMB0682	<i>pyrC</i>	dihydroorotase (DHOase)	1,73		

NMB0683	<i>nusB</i>	N utilization substance protein B (NusB protein)	1,65		
NMB0684	<i>ribH</i>	6,7-dimethyl-8-ribityllumazine synthase	1,22		
NMB0686	<i>rnc</i>	ribonuclease III (RNase III)	2,27		
NMB0688	<i>trpF</i>	N-(5'-phosphoribosyl)anthranilate isomerase (PRAI)	1,40		
NMB0690	<i>purF</i>	amidophosphoribosyltransferase		-1,01	
NMB0696		putative ABC transporter ATP-binding protein	0,93		
NMB0698		putative DNA glycosylase	-1,92	-1,10	
NMB0705		putative transporter	-2,89	-1,52	
NMB0718	<i>hemH</i>	ferrochelatase (protoheme ferro-lyase; heme synthetase)	1,52		
NMB0721	<i>infC</i>	translation initiation factor IF-3	1,47		
NMB0722	<i>rpmI</i>	50S ribosomal protein L35		0,56	-0,68
NMB0725		putative type II restriction-modification system enzyme Mod	-1,98		
NMB0734		conserved hypothetical protein	1,15		
NMB0736		putative phosphotransferase enzyme IIA component (PTS system EIIA component)		-0,97	1,08
NMB0737	<i>hprK</i>	HPr kinase/phosphorylase (HPrK/P; HPr(Ser) kinase/phosphorylase)		-0,83	
NMB0743	<i>ubiE</i>	ubiquinone/menaquinone biosynthesis methyltransferase UbiE	1,47		
NMB0748	<i>hfq</i>	Hfq protein			0,86
NMB0750		putative peroxiredoxin Bcp (thioredoxin reductase; bacterioferritin comigratory protein homolog)			-0,83
NMB0753		putative thioredoxin	-2,30	-1,26	-1,56
NMB0757	<i>purC</i>	phosphoribosylaminoimidazole-succinocarboxamide synthase (SAICAR synthetase)	-0,85		
NMB0758	<i>pnp</i>	polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase; PNPase; CAP87K)	2,00		
NMB0759		conserved hypothetical integral membrane protein	-1,39		
NMB0760	<i>dapF</i>	diaminopimelate epimerase (DAP epimerase)	0,89		
NMB0763	<i>cysK</i>	cysteine synthase A (O-acetylserine sulfhydrylase A; O-acetylserine (thiol)-lyase A; CSase A)		-1,44	
NMB0765	<i>lepB</i>	signal peptidase I (SPase I; leader peptidase I)			0,97
NMB0766		putative GTP-binding protein LepA	0,95		
NMB0771		putative deoxyribonuclease	1,30		
NMB0777	<i>hemD</i>	uroporphyrinogen-III synthase	-0,97		
NMB0780		conserved hypothetical protein	0,93		
NMB0787		putative amino acid ABC transporter binding lipoprotein	1,34		
NMB0788		putative amino acid ABC transporter permease protein	1,88		1,39
NMB0799	<i>rrmJ</i>	ribosomal RNA large subunit methyltransferase J		0,85	
NMB0804		putative NAD(P)H nitroreductase		-1,08	
NMB0809		conserved hypothetical protein	1,22		1,29
NMB0811	<i>murB</i>	UDP-N-acetylenolpyruvoylglicosamine reductase	1,14		
NMB0817		hypothetical protein	-2,04		
NMB0819		hypothetical protein	-1,45		
NMB0822		putative HtpX-like protease	2,32	1,82	
NMB0826		putative type II restriction-modification system enzyme Mod	-2,28	-1,54	
NMB0832		putative anticodon nuclease	-2,48		

NMB0834		IS1655 transposase		0,91	
NMB0838		putative cold shock protein		-1,20	
NMB0841		hypothetical integral membrane protein			1,33
NMB0843	<i>pcnB</i>	poly(A) polymerase (PAP; plasmid copy number protein)	1,24		
NMB0849	<i>dcd</i>	deoxycytidine triphosphate deaminase (dCTP deaminase)	1,13		
NMB0850		hypothetical periplasmic protein	1,24		
NMB0851	<i>rdgC</i>	recombination associated protein RdgC	1,39		
NMB0852		putative GTP-binding protein EngA	1,55		
NMB0853		conserved hypothetical TPR-containing membrane protein	1,02		
NMB0855		putative peptidase	-0,94		
NMB0856		hypothetical protein	-3,16		
NMB0857		hypothetical protein	-1,60	-1,57	
NMB0858		hypothetical protein	-2,11		
NMB0859		hypothetical protein	-2,83	-1,66	
NMB0860		hypothetical protein	-2,66	-1,71	
NMB0861		hypothetical integral membrane protein	-2,48		
NMB0863		hypothetical integral membrane protein	-2,51	-3,02	
NMB0865		hypothetical integral membrane protein	-1,42	-2,20	
NMB0866		conserved hypothetical outer-membrane protein	-1,64	-2,82	1,62
NMB0867		putative RNA pseudouridine synthase	-1,22		-0,80
NMB0870	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	1,45		0,95
NMB0876	<i>rplY</i>	50S ribosomal protein L25	1,45		
NMB0877	<i>dacC</i>	D-alanyl-D-alanine carboxypeptidase (DD-peptidase; DD-carboxypeptidase; CPase; PBP5)			-1,26
NMB0879	<i>cysA</i>	sulfate/thiosulfate import ATP-binding protein CysA (sulfate-transporting ATPase)	2,58	2,06	
NMB0880	<i>cysW</i>	sulfate transport system permease protein CysW	2,55	2,16	
NMB0882		hypothetical protein	-1,26		
NMB0883		conserved hypothetical integral membrane protein			-1,91
NMB0885	<i>dnaB</i>	replicative DNA helicase	0,92	0,60	
NMB0890	<i>pilX</i>	minor pilin PilX		-1,27	
NMB0897		conserved hypothetical protein			0,97
NMB0900		putative KilA-N domain-containing protein	1,86	1,63	
NMB0901		conserved hypothetical protein	-1,42		
NMB0902		hypothetical protein			-2,29
NMB0904		hypothetical periplasmic protein			-2,31
NMB0905		hypothetical protein	-1,47		-2,35
NMB0906		conserved hypothetical protein	-1,76		
NMB0907		conserved hypothetical protein	-2,49		
NMB0908		hypothetical protein			-2,05
NMB0911		IS1655 transposase		1,03	-0,81
NMB0914		putative PemI-like protein	-1,51		

NMB0923	<i>cytC</i>	cytochrome c'		1,17
NMB0924		putative oxidoreductase	-1,27	
NMB0935	<i>miaA</i>	tRNA delta(2)-isopentenylpyrophosphate transferase	1,90	
NMB0941	<i>rpmJ</i>	50S ribosomal protein L36		-1,35
NMB0943	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	1,21	
NMB0952		conserved hypothetical TPR-containing protein	-1,01	
NMB0960	<i>sucD</i>	succinyl-CoA synthetase alpha chain (SCS-alpha)		-0,78
NMB0961		conserved hypothetical protein	-0,93	0,94
NMB0962	<i>uvrA</i>	UvrABC system protein A (UvrA protein; excinuclease ABC subunit A)	1,41	0,87
NMB0964		putative TonB-dependent receptor	-1,80	-0,87
NMB0966	<i>trpG</i>	anthranilate synthase component II (glutamine amido-transferase)	-1,26	
NMB0975		hypothetical protein	-3,17	-1,87
NMB0978	<i>pntB</i>	NAD(P) transhydrogenase subunit beta	-1,69	
NMB0980	<i>pntA</i>	NAD(P) transhydrogenase subunit alpha	-1,43	
NMB0981	<i>serB</i>	phosphoserine phosphatase		-1,00
NMB0985		conserved hypothetical phage protein	1,86	0,90
NMB0994		putative acyl-CoA dehydrogenase	2,62	
NMB0995		conserved hypothetical protein	2,21	
NMB0997	<i>dld</i>	D-lactate dehydrogenase		-1,60
NMB0998		putative oxidoreductase	0,84	1,00
NMB1007		putative DNA-binding phage protein	-1,26	
NMB1011		conserved hypothetical protein	-0,96	
NMB1033	<i>nlaIVM</i>	type II restriction-modification system modification methylase NlaIV	-1,59	
NMB1037		putative glutamate--cysteine ligase (gamma-glutamylcysteine synthetase)	-1,57	
NMB1042		putative cation-transporting ATPase	-1,43	-1,18
NMB1045		conserved hypothetical protein	2,14	
NMB1046	<i>thrC</i>	threonine synthase	1,53	0,87
NMB1048		putative transporter	4,64	3,62
NMB1051		putative ABC transporter ATP-binding protein		1,37
NMB1052	<i>dedA</i>	DedA protein (DSG-1 protein)	1,31	
NMB1055	<i>glyA</i>	serine hydroxymethyltransferase (serine methylase; SHMT)		1,47
NMB1057	<i>ggt</i>	gamma-glutamyltranspeptidase	-0,93	-1,01
NMB1059		conserved hypothetical protein	-2,62	-1,70
NMB1063	<i>folB</i>	dihydronopterin aldolase (DHNA)	-1,55	-1,16
NMB1064	<i>nudF</i>	ADP-ribose pyrophosphatase	-1,57	
NMB1071		conserved hypothetical protein		-1,12
NMB1072	<i>lgt</i>	prolipoprotein diacylglycerol transferase	-1,54	-1,36
NMB1077		truncated putative ABC transporter ATP-binding protein (C-terminal 30% of the protein)	2,35	
NMB1084		hypothetical protein	-2,85	-2,27
NMB1088		conserved hypothetical protein	-2,90	-1,76

NMB1099		IS1655 transposase	0,94		
NMB1101		putative Gp36-like prophage protein	2,01		
NMB1102		putative Gp37-like prophage protein	1,94		
NMB1103		conserved hypothetical protein	2,79		
NMB1104		putative bacteriophage Mu-like tail sheath protein	2,41		
NMB1105		conserved hypothetical protein	2,30		
NMB1107		hypothetical lipoprotein	-2,51		
NMB1115		putative phage tail fibre protein		-2,18	
NMB1118		conserved hypothetical protein	-1,45		
NMB1124		conserved hypothetical lipoprotein	-2,04	-1,49	
NMB1125		conserved hypothetical TPR-containing lipoprotein	-2,02	-0,92	
NMB1126		putative CsgG-like lipoprotein	-2,16	-1,37	
NMB1127		putative oxidoreductase	-1,81		
NMB1138		putative RNA-binding protein	-1,11		
NMB1140	<i>tilS</i>	tRNA(Ile)-lysidine synthetase	2,08		1,23
NMB1158		putative cytochrome	1,43		
NMB1199		putative GTP-binding protein TypA	0,79		
NMB1200	<i>rnr</i>	ribonuclease R (RNase R; VacB protein)		-1,14	
NMB1201	<i>guaB</i>	inosine-5'-monophosphate dehydrogenase	1,29		
NMB1202		hypothetical protein	-2,68	-1,70	-1,64
NMB1212		hypothetical lipoprotein	-2,72		
NMB1213		hypothetical lipoprotein	-2,75		
NMB1214	<i>tpsA3</i>	haemagglutinin/hemolysin-related protein TpsA3 lipoyl synthase (lipoic acid synthase; lipoate synthase; lipoyl-acyl-carrier protein synthase; sulfur insertion protein LipA2; lip-syn)	-2,82		
NMB1216	<i>lipA</i>	hypothetical integral membrane protein	0,81		
NMB1224		conserved hypothetical periplasmic protein	-2,35	-2,06	-1,06
NMB1225		hypothetical periplasmic protein	-1,34	-0,72	-1,04
NMB1229		hypothetical periplasmic protein			-1,11
NMB1236		hypothetical periplasmic protein	-1,77		-1,07
NMB1239		conserved hypothetical protein	-1,88		
NMB1241	<i>cca</i>	multifunctional CCA protein	1,78		1,44
NMB1242		conserved hypothetical protein	1,33		
NMB1243	<i>ruvB</i>	Holliday junction DNA helicase RuvB	1,53		
NMB1254	<i>ribA</i>	GTP cyclohydrolase II	0,94		
NMB1256	<i>ribAB</i>	bifunctional riboflavin biosynthesis protein	1,11		
NMB1265		conserved hypothetical protein	-1,68	-0,82	-0,77
NMB1266		putative cation uptake HTH-type transcriptional regulator	-1,60		
NMB1267		putative low molecular weight protein-tyrosine-phosphatase	-1,02		
NMB1268	<i>glxK</i>	glycerate kinase	-1,60		
NMB1269		conserved hypothetical protein		-1,25	

NMB1280		putative acyl-CoA dehydrogenase			1,53
NMB1281	<i>mfd</i>	transcription-repair coupling factor (TRCF)	1,70		
NMB1283	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase	1,75		
NMB1284		conserved hypothetical integral membrane protein	1,46		1,17
NMB1285	<i>eno</i>	enolase (2-phosphoglycerate hydratase; 2-phospho-D-glycerate hydro-lyase)		-1,30	1,01
NMB1286		putative cell division protein FtsB		-1,16	
NMB1289		putative type II restriction-modification system enzyme Res	-1,75	-1,18	-1,01
NMB1290		putative type II restriction-modification system enzyme Mod	-2,33		
NMB1300	<i>cmk</i>	cytidylate kinase (CK; cytidine monophosphate kinase; CMP kinase)	1,54		
NMB1301	<i>rpsA</i>	30S ribosomal protein S1	1,81		
NMB1302	<i>ihfB</i>	integration host factor beta-subunit (IHF-beta)	1,52		
NMB1303		putative HTH-type transcriptional regulator	-1,36		-1,14
NMB1304		putative alcohol dehydrogenase class III	1,57	1,30	
NMB1305		putative esterase	1,76	1,13	
NMB1306		putative ATPase	1,54	1,08	
NMB1308		conserved hypothetical protein	1,19	1,12	
NMB1309	<i>pilW</i>	type IV pilus biogenesis lipoprotein PilW	1,32		
NMB1310	<i>ispG</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	1,53		1,44
NMB1314	<i>ftsK</i>	DNA translocase FtsK	1,55		
NMB1315		putative uracil permease (uracil transporter)	1,37		
NMB1320	<i>rplI</i>	50S ribosomal protein L9	1,89		
NMB1322	<i>priB</i>	primosomal replication protein n		0,57	-0,51
NMB1323	<i>rpsF</i>	30S ribosomal protein S6			-0,49
NMB1324	<i>trxR</i>	thioredoxin reductase (TRXR)	0,71		
NMB1328	<i>trmB</i>	tRNA (guanine-N(7)-)methyltransferase (tRNA(m7G46)-methyltransferase)	1,35	0,85	
NMB1332	<i>prc</i>	carboxy-terminal processing protease (C-terminal processing protease)		-0,58	
NMB1335		conserved hypothetical protein	-0,73		
NMB1342	<i>aceF</i>	dihydrolipoyllysine-residue acetyltransferase			0,92
NMB1347	<i>suhB</i>	inositol-1-monophosphatase (IMPase; inositol-1-phosphatase; I-1-Pase)	1,62		
NMB1350		hypothetical protein	-1,87		
NMB1353		putative aldehyde dehydrogenase-like protein	1,38	0,73	
NMB1356	<i>gatA</i>	aspartyl-tRNA(Asn) amidotransferase subunit A (Asp-ADT subunit A)			1,55
NMB1357		conserved hypothetical protein	1,22		
NMB1358	<i>gatB</i>	aspartyl-tRNA(Asn) amidotransferase subunit B (Asp-ADT subunit B)	1,05		
NMB1361	<i>rluB</i>	ribosomal large subunit pseudouridine synthase B	1,99		
NMB1362		putative transporter	1,55		1,56
NMB1363	<i>xseA</i>	exodeoxyribonuclease VII large subunit (exonuclease VII large subunit)	1,19		1,41
NMB1364	<i>nadE</i>	NH(3)-dependent NAD(+) synthetase	-1,12		
NMB1366	<i>trxA</i>	thioredoxin (TRX)	-1,05		
NMB1368		putative ATP-dependent RNA helicase	4,05	3,63	

NMB1370		conserved hypothetical protein		1,66	1,53	
NMB1372	<i>clpX</i>	ATP-dependent Clp protease ATP-binding subunit ClpX		-2,94		-1,88
NMB1373	<i>rbfA</i>	ribosome-binding factor A		2,00		1,36
NMB1374	<i>truB</i>	tRNA pseudouridine synthase B		2,17		1,30
NMB1381		putative IscA-like protein		1,05	0,93	
NMB1383	<i>hscB</i>	co-chaperone protein Hsc20		1,39		0,80
NMB1389	<i>hexR</i>	HTH-type transcriptional repressor HexR (hex regulon repressor)		0,67		
NMB1394	<i>eda</i>	KHG/KDPG aldolase		1,98		
NMB1396	<i>mutY</i>	A/G-specific adenine glycosylase		1,31		
NMB1398	<i>sodC</i>	superoxide dismutase [Cu-Zn]		-3,53		
NMB1402		hypothetical integral membrane protein		-3,39		
NMB1403		FrpA/C-like protein		-2,31		
NMB1404		hypothetical integral membrane protein		-1,05		
NMB1408		conserved hypothetical integral membrane protein		-2,40		
NMB1409		putative FrpA/FrpC cassette		-2,34		-1,88
NMB1411		IS1016 group transposase		-1,27		
NMB1414	<i>frpD</i>	FrpA/C-binding lipoprotein			-1,78	
NMB1423		conserved hypothetical protein		-1,02		
NMB1430	<i>greA</i>	transcription elongation factor GreA (transcript cleavage factor GreA)		1,74	1,50	
NMB1432	<i>aroA</i>	3-phosphoshikimate 1-carboxyvinyltransferase		1,83		1,52
NMB1437		conserved hypothetical protein		1,28	1,66	
NMB1438		putative ferredoxin-like protein		1,21	1,42	
NMB1439	<i>purE</i>	phosphoribosylaminoimidazole carboxylase catalytic subunit (AIR carboxylase; AIRC)		-1,01		
NMB1442	<i>mutL</i>	DNA mismatch repair protein MutL			1,17	
NMB1444		conserved hypothetical protein			-0,79	
NMB1447	<i>rep</i>	ATP-dependent DNA helicase Rep				0,98
NMB1458	<i>fumC</i>	fumarate hydratase class II (fumarase C)		-1,22		
NMB1474		putative tautomerase		-1,37		
NMB1475		conserved hypothetical periplasmic protein		-3,81	-2,74	-1,66
NMB1483		putative metallopeptidase		-2,33		-2,12
NMB1484	<i>surE</i>	5'-nucleotidase SurE (nucleoside 5'-monophosphate phosphohydrolase)			-0,98	
NMB1487		conserved hypothetical protein		1,40		
NMB1488	<i>gabD</i>	succinate-semialdehyde dehydrogenase [NADP+] (SSDH)		1,89		
NMB1493		putative carbon starvation protein A		-2,04	-2,36	
NMB1494		conserved hypothetical protein			-2,37	
NMB1505	<i>pncB</i>	nicotinate phosphoribosyltransferase (NAPRTase)		1,58		
NMB1509		putative amino acid ABC transporter permease protein		-1,30		
NMB1510		putative periplasmic nuclease		-1,62		
NMB1514	<i>dnaQ</i>	DNA polymerase III epsilon subunit		-0,90		
NMB1518	<i>ackA</i>	acetate kinase 1 (acetokinase 1)			-1,43	

NMB1522		putative FKBP-type peptidyl-prolyl cis-trans isomerase (PPIase; rotamase)	-1,88		
NMB1527	<i>rfaF</i>	ADP-heptose:LPS heptosyltransferase II	2,10	1,29	
NMB1528		methylated-DNA--protein-cysteine methyltransferase	1,06	1,04	
NMB1533		H.8 outer-membrane lipoprotein		-1,00	
NMB1536	<i>secA</i>	preprotein translocase SecA subunit	1,34		
NMB1537	<i>dnaG</i>	DNA primase	1,07	1,23	
NMB1538	<i>rpoD</i>	RNA polymerase sigma factor RpoD (Sigma-70)	-0,87		-1,04
NMB1540	<i>lbpA</i>	lactoferrin-binding protein A (LbpA)	-3,31	-3,07	
NMB1541	<i>lbpB</i>	lactoferrin-binding protein B (LbpB)	-4,56	-4,32	
NMB1544		conserved hypothetical protein			-0,93
NMB1545		hypothetical protein	-3,28	-2,11	
NMB1548		putative TspB protein	-1,66	-1,15	
NMB1550		conserved hypothetical integral membrane protein	-1,98		
NMB1552		putative pilin gene-inverting protein (PIVML)	-2,56		
NMB1556	<i>trmU</i>	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	-0,96		
NMB1557		conserved hypothetical periplasmic protein	-1,16		
NMB1560	<i>glnS</i>	glutaminyl-tRNA synthetase (glutamine--tRNA ligase; GlnRS)	1,26	1,05	0,79
NMB1562		conserved hypothetical integral membrane protein	1,47		
NMB1563		putative HTH-type transcriptional regulator	-1,15		
NMB1564		putative OsmC-like protein	-0,91	-0,60	-0,67
NMB1572	<i>acnB</i>	aconitate hydratase 2 (citrate hydro-lyase 2; aconitase 2)		1,74	-1,22
NMB1574	<i>ilvC</i>	ketol-acid reductoisomerase			0,74
NMB1576	<i>ilvH</i>	acetolactate synthase small subunit		0,82	
NMB1579	<i>hisG</i>	ATP phosphoribosyltransferase (ATP-PRTase; ATP-PRT)		0,81	
NMB1580		conserved hypothetical protein		0,38	
NMB1587		putative peptidase	2,05	1,91	
NMB1593		conserved hypothetical integral membrane protein	1,46		
NMB1594		putative spermidine/putrescine-binding lipoprotein		-1,03	
NMB1597		conserved hypothetical integral membrane protein	-0,96		
NMB1602		truncated IS110 family transposase	1,25		
NMB1604	<i>gpm</i>	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	-2,35		-1,27
NMB1617		putative tellurite resistance protein TehB	-1,54		-1,48
NMB1628		putative TspB protein	-2,14		
NMB1629		conserved hypothetical protein	-2,61		
NMB1633		conserved hypothetical protein	-3,44	-2,15	
NMB1637		putative nitroreductase	-1,06		
NMB1638		putative sulfatase	-1,65	-1,69	
NMB1641		conserved hypothetical protein	2,43	1,84	
NMB1642	<i>nusA</i>	transcription elongation protein nusA	1,08	1,34	
NMB1646		putative hemolysin III (Hly-III)			-0,94

NMB1651	<i>alr</i>	alanine racemase		2,94	2,58	
NMB1652		conserved hypothetical protein		-1,37	-1,43	
NMB1653		conserved hypothetical protein		-1,26	-0,65	-0,63
NMB1657	<i>comE2</i>	DNA-binding competence protein ComE2			0,75	-0,68
NMB1658	<i>coaBC</i>	coenzyme A biosynthesis bifunctional protein CoaBC s			1,05	
NMB1664		putative peptidase		1,95	1,47	
NMB1665		conserved hypothetical protein		-2,14		-1,48
NMB1668	<i>hpuB</i>	hemoglobin-haptoglobin utilization protein B		-1,79	-1,65	
NMB1669	<i>hemO</i>	heme oxygenase HemO		-2,68	-2,71	
NMB1670		conserved hypothetical integral membrane protein		1,98	1,32	
NMB1671		conserved hypothetical protein			1,25	
NMB1675		hypothetical integral membrane protein			0,81	
NMB1680	<i>aroC</i>	chorismate synthase		1,13		
NMB1687		putative deoxyribonuclease			0,84	
NMB1688		putative L-asparaginase I				2,06
NMB1689		putative DedA-family integral membrane protein			1,10	
NMB1690	<i>glmM</i>	phosphoglucosamine mutase				1,02
NMB1696		putative acyl carrier protein (ACP)		-4,13		
NMB1697		putative acyl carrier protein (ACP)		-3,58		
NMB1698		putative acyltransferase		-1,33		
NMB1702	<i>fabG</i>	3-oxoacyl-[acyl-carrier-protein] reductase		-0,67		
NMB1710	<i>gdhA</i>	NADP-specific glutamate dehydrogenase (NADP-GDH)			-1,69	1,31
NMB1712		putative L-lactate permease-related protein		-2,49		
NMB1714	<i>mtrE</i>	outer-membrane lipoprotein MtrE			1,69	
NMB1715	<i>mtrD</i>	drug efflux transport protein MtrD			1,76	
NMB1718		hypothetical protein		-2,10		
NMB1727		conserved hypothetical protein			-1,38	
NMB1733		hypothetical integral membrane protein			-1,36	
NMB1734	<i>grxB</i>	glutaredoxin 2 (Grx2)		-1,62		-1,17
NMB1739		hypothetical integral membrane protein			-3,50	
NMB1744		hypothetical integral membrane protein			-2,45	
NMB1753		putative VapD-like protein		-3,09	-1,77	
NMB1755		hypothetical protein		-2,72	-1,36	
NMB1756		hypothetical protein		-2,09		
NMB1759		conserved hypothetical protein		-2,17		
NMB1761		conserved hypothetical protein		-2,02		
NMB1764		hypothetical lipoprotein		-1,93		
NMB1765		hypothetical periplasmic protein		-2,17		
NMB1768	<i>tpsA</i>	haemagglutinin/hemolysin-related protein TpsA2		-2,36	-1,23	-1,31
NMB1771		hypothetical integral membrane protein		-2,13		

NMB1772	<i>tpsS7</i>	putative TpsS7 cassette	-2,15		
NMB1777		conserved hypothetical protein	-2,66		
NMB1779	<i>tpsA</i>	haemagglutinin/hemolysin-related protein TpsA3	-1,68		
NMB1780	<i>tpsB</i>	TpsA3 activation/secretion protein TpsB3	-1,58	-1,36	
NMB1782		hypothetical protein	-1,52		
NMB1785		hypothetical lipoprotein	-1,80		
NMB1787	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase	1,09	1,06	
NMB1794		putative transporter	-0,99		
NMB1796		putative oxidoreductase		-1,66	1,14
NMB1809	<i>pilN</i>	type IV pilus biogenesis protein PilN		-0,78	
NMB1810	<i>pilO</i>	type IV pilus biogenesis protein PilO		-0,76	
NMB1811	<i>pilP</i>	type IV pilus biogenesis lipoprotein PilP		-0,56	
NMB1813	<i>aroK</i>	shikimate kinase (SK)	1,31		
NMB1814	<i>aroB</i>	3-dehydroquinate synthase	1,71		1,91
NMB1815		putative class-II glutamine amidotransferase	1,75		1,27
NMB1817	<i>ribD</i>	riboflavin biosynthesis protein RibD			1,31
NMB1819		hypothetical periplasmic protein	0,97		
NMB1826		conserved hypothetical protein	-1,17	-0,88	
NMB1827	<i>dnaE</i>	DNA polymerase III alpha subunit		1,77	
NMB1834	<i>ribF</i>	riboflavin biosynthesis protein RibF	1,36	1,03	
NMB1838		putative GTP-dependent nucleic acid-binding protein EngD	1,37		
NMB1839	<i>fhs</i>	formate--tetrahydrofolate ligase	1,15		
NMB1841		putative sugar-phosphate nucleotidyl transferase	2,50		
NMB1842		putative 4-hydroxyphenylacetate 3-monooxygenase, reductase component	2,08	1,81	
NMB1843		putative HTH-type transcriptional regulator		0,81	
NMB1845		putative membrane-associated thioredoxin	2,81	2,83	
NMB1846		putative ATP-binding protein	1,83		0,99
NMB1854		conserved hypothetical protein			-1,35
NMB1859	<i>queA</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase			-0,95
NMB1860	<i>accB</i>	biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP)	0,77		
NMB1862	<i>prmA</i>	ribosomal protein L11 methyltransferase (L11 Mtase)	1,65		1,48
NMB1863	<i>orn</i>	oligoribonuclease	1,63		
NMB1866		putative MiaB-like tRNA modification enzyme	2,38	2,77	
NMB1872		putative acetyltransferase	1,28		
NMB1875		conserved hypothetical protein			0,97
NMB1884		putative thiosulfate sulfurtransferase		-1,70	
NMB1885	<i>pcm</i>	protein-L-isoaspartate O-methyltransferase		-0,77	
NMB1890		conserved hypothetical protein			-2,03
NMB1891		putative DNA-binding protein			-1,85
NMB1899		hypothetical periplasmic protein	-0,85		-0,74

NMB1902	<i>dnaN</i>	DNA polymerase III beta subunit		-0,79
NMB1906		conserved hypothetical protein	2,26	1,23
NMB1909		putative Maf-like protein	1,11	1,05
NMB1912		putative phosphoribosyltransferase	0,82	
NMB1913	<i>plsX</i>	fatty acid/phospholipid synthesis protein PlsX	1,43	0,92
NMB1919	<i>msbA</i>	lipid A export ATP-binding/permease protein MsbA	1,72	
NMB1920	<i>guaA</i>	GMP synthase		1,26
NMB1929	<i>lgtA</i>	fragment of lacto-N-neotetraose biosynthesis glycosyl tranferase LgtA	1,35	
NMB1934	<i>atpD</i>	ATP synthase beta chain		1,18
NMB1935	<i>atpG</i>	ATP synthase gamma chain		-1,08
NMB1936	<i>atpA</i>	ATP synthase alpha chain		-1,12
NMB1937	<i>atpH</i>	ATP synthase delta chain		-0,75
NMB1938	<i>atpF</i>	ATP synthase B chain		-1,15
NMB1939	<i>atpE</i>	ATP synthase C chain (lipid-binding protein; dicyclohexylcarbodiimide-binding protein)		-1,23
NMB1941		putative ATP synthase protein I		-0,99
NMB1947		putative D-methionine transport system permease protein MetI	2,42	2,54
NMB1948		putative D-methionine transport system ATP-binding protein MetN	2,17	2,58
NMB1954		conserved hypothetical integral membrane protein	-2,14	-2,22
NMB1955		putative transporter	-2,56	-2,76
NMB1956	<i>rpmE</i>	50S ribosomal protein L31	1,00	1,23
NMB1960		conserved hypothetical protein	1,11	
NMB1962		conserved hypothetical protein	1,61	
NMB1964		conserved hypothetical integral membrane protein	1,27	
NMB1965		conserved hypothetical membrane protein	0,99	
NMB1967		putative HTH-type transcriptional regulator	-2,62	
NMB1968	<i>aldA</i>	aldehyde dehydrogenase A (lactaldehyde dehydrogenase)	-1,95	
NMB1971		conserved hypothetical TPR-containing membrane-associated protein	-1,42	
NMB1973	<i>groS</i>	10 kDa chaperonin (protein Cpn10; GroES protein)		-0,90
NMB1975		putative sodium-dependent transporter	-1,91	
NMB1978		putative CyA-like protein	-1,94	-1,29
NMB1982	<i>polA</i>	DNA polymerase I (POL I)	-1,60	-1,42
NMB1983		conserved hypothetical protein	-1,59	
NMB1986		conserved hypothetical integral membrane protein		0,93
NMB1988	<i>fetA</i>	TonB-dependent enterobactin receptor FetA (FrpB)		-1,64
NMB1989	<i>fetB</i>	enterobactin uptake system binding lipoprotein FetB		-1,25
NMB1990		putative ferric enterobactin uptake system permease FetD	1,31	
NMB1996	<i>purL</i>	phosphoribosylformylglycinamide synthase	1,31	1,47
NMB1997		putative hydroxyacylglutathione hydrolase (glyoxalase II; Glx II)	1,62	1,23
NMB1999		putative divalent cation transporter		1,17
NMB2000	<i>hslO</i>	33 kDa chaperonin (heat shock protein 33 homolog; HSP33)	-1,51	

NMB2005	<i>argJ</i>	arginine biosynthesis bifunctional protein ArgJ	-1,66		
NMB2008		putative ABC transporter ATP-binding protein	-2,74		
NMB2012		putative HTH-type transcriptional regulator	-1,32		
NMB2013		conserved hypothetical protein	-1,15		
NMB2015		conserved hypothetical protein	-2,47		-2,85
NMB2016	<i>comP</i>	minor pilin ComP	-1,64	-1,69	
NMB2017	<i>comE3</i>	DNA-binding competence protein ComE3		-1,25	0,77
NMB2021		putative Fe(2+) trafficking protein	-0,79	-1,21	
NMB2023		conserved hypothetical protein		-0,55	
NMB2030	<i>ubiG</i>	3-demethylubiquinone-9 3-methyltransferase	1,29	0,74	
NMB2033	<i>gmhB</i>	D,D-heptose 1,7-bisphosphate phosphatase	1,83	1,58	
NMB2034	<i>nlaB</i>	1-acyl-sn-glycerol-3-phosphate acyltransferase NlaB	1,56		
NMB2035		conserved hypothetical protein	1,73	1,21	
NMB2037		putative PemI-like protein	-1,26		-1,51
NMB2040	<i>thiC</i>	thiamine biosynthesis protein ThiC	-1,56		
NMB2042		putative ABC transporter ATP-binding protein	1,71		
NMB2047	<i>hpt</i>	hypoxanthine-guanine-xanthine phosphoribosyltransferase			0,93
NMB2048		putative periplasmic DNA ligase (polydeoxyribonucleotide synthase [ATP])	1,25		1,99
NMB2058		conserved hypothetical protein	-1,02		-1,16
NMB2059		conserved hypothetical protein	-1,09		-0,89
NMB2060	<i>gpsA</i>	glycerol-3-phosphate dehydrogenase	-0,77		
NMB2061	<i>ppc</i>	phosphoenolpyruvate carboxylase (PEPCase; PEPC)			1,64
NMB2063		putative SlyX-like protein	-1,43		
NMB2065		putative protein methyltransferase HemK	0,73		
NMB2066		putative TldD-like peptidase	1,11		1,05
NMB2068		putative FAD-dependent oxidoreductase	-1,25	-1,50	0,69
NMB2070		putative ThiS-like protein	-2,73		
NMB2071	<i>thiG</i>	thiazole biosynthesis protein ThiG	-2,19		
NMB2074		conserved hypothetical periplasmic protein	1,29	0,82	
NMB2075		putative BirA-like multifunctional protein	2,45	1,54	1,08
NMB2076	<i>rfaE</i>	D-beta-D-heptose 1-phosphate adenosyltransferase	1,50	1,24	1,17
NMB2082		putative exodeoxyribonuclease			1,16
NMB2085		putative ATP-binding protein	-1,05		
NMB2086		putative GTP-binding protein		0,93	
NMB2088		putative methyltransferase		1,84	
NMB2090	<i>gmhA</i>	phosphoheptose isomerase (sedoheptulose 7-phosphate isomerase)		0,94	
NMB2093	<i>map</i>	methionine aminopeptidase (MAP; peptidase M)			0,76
NMB2095		conserved hypothetical protein		0,93	
NMB2096	<i>mqa</i>	malate:quinone oxidoreductase (malate dehydrogenase [acceptor]; MQO)	-1,21		
NMB2099		putative 5-formyltetrahydrofolate cyclo-ligase (methenyl-THF synthetase)	-1,42		-0,94

NMB2106	hypothetical protein	-2,55
NMB2108	hypothetical protein	-1,68
NMB2109	conserved hypothetical protein	-1,56
NMB2110	conserved hypothetical protein	-1,40
NMB2112	hypothetical protein	-2,33
NMB2113	hypothetical protein	-2,01
NMB2115	hypothetical protein	-2,16
NMB2116	hypothetical protein	-1,88
NMB2118	hypothetical protein	-1,78
NMB2119	<i>mafS5</i> putative MafS5 cassette	-1,75
NMB2120	hypothetical protein	-2,18
NMB2121	hypothetical protein	-1,91
NMB2123	hypothetical protein	-1,39
NMB2125	conserved hypothetical protein	-1,94
NMB2127	putative peptidase	-1,39
NMB2132	transferrin-binding protein-like lipoprotein (lipoprotein GNA2132)	-1,19
NMB2133	putative transporter	-1,45
NMB2134	conserved hypothetical outer-membrane protein	0,90
NMB2140	conserved hypothetical integral membrane protein	1,36
NMB2144	putative ECF-family RNA polymerase sigma factor	0,98
NMB2147	conserved hypothetical lipoprotein	0,90
NMB2148	IS1655 transposase	0,97
NMB2150	putative RNA-binding protein	1,87
NMB2151	<i>purD</i> phosphoribosylamine--glycine ligase	0,74
NMB2152	hypothetical protein	-3,09
NMB2153	conserved hypothetical protein	1,52
NMB2154	<i>etfA</i> electron transfer flavoprotein alpha-subunit	-1,10
NMB2159	<i>gapB</i> glyceraldehyde-3-phosphate dehydrogenase B (GAPDH)	-0,90
		-1,58

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